

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2002, 22:06:22 ; Search time 17398.4 Seconds

(without alignments)
1042.620 Million cell updates/sec

Title: US-09-303-518D-131

Perfect score: 1344

Sequence: 1 atgattaaatcaaaaaagg.....ccattgagaagaagcgtga 1344

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST:*
1: em_estba:*
2: em_estba:*
3: em_estba:*
4: em_estba:*
5: em_estba:*
6: em_estba:*
7: em_estba:*
8: em_estba:*
9: em_estba:*
10: em_estba:*
11: em_estba:*
12: em_estba:*
13: em_estba:*
14: em_estba:*
15: em_estba:*
16: em_estba:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	110.2	8.2	349	12	CNS076YI
2	39.2	2.9	528	10	BG606950
3	38.6	2.9	458	9	AW174071
4	38.2	2.8	407	9	AW172028
5	38.2	2.8	684	10	B1728886
6	38	2.8	384	9	AI392198
7	37.4	2.8	434	10	BG578214
8	37.4	2.8	621	10	BG578214
9	37.2	2.8	320	9	AV938950
10	37.2	2.8	376	10	BF293584
11	37.2	2.8	577	9	AV938949
12	37	2.8	378	10	D47749
13	37	2.8	497	12	P947R
14	36.8	2.7	606	9	AA538611
15	36.6	2.7	632	10	BE775370
16	36.6	2.7	890	10	BI949615
17	36.4	2.7	216	10	BE360609

18	36.2	2.7	328	10	BE424405
19	36.2	2.7	407	10	BF428970
20	36.2	2.7	460	10	BG262553
21	36.2	2.7	460	10	BE590713
22	36.2	2.7	475	10	BE775489
23	36.2	2.7	505	9	AA614629
24	36.2	2.7	578	9	AL508674
25	36.2	2.7	595	10	BI479848
26	36.2	2.7	625	10	BE590921
27	36.2	2.7	639	10	BG650187
28	36.2	2.7	893	9	AL523270
29	36.2	2.7	921	10	BI147211
30	36.2	2.7	943	9	AL556080
31	36	2.7	349	9	AJ282139
32	36	2.7	357	9	AJ282150
33	35.8	2.7	321	12	AO966942
34	35.8	2.7	574	10	BI949252
35	35.8	2.7	615	10	BG579193
36	35.8	2.7	630	10	BG521603
37	35.6	2.6	152	10	BF769109
38	35.6	2.6	344	10	C26554
39	35.6	2.6	394	12	A2049430
40	35.6	2.6	506	9	AI399239
41	35.6	2.6	779	10	BI464724
42	35.4	2.6	336	10	D47324
43	35.4	2.6	613	10	BG577607
44	35.2	2.6	580	10	BG262171
45	35.2	2.6	687	12	AG184405
46	35.2	2.6	323	9	AI368671
47	35	2.6	361	10	BE776874
48	35	2.6	364	10	BE285901
49	35	2.6	433	9	AM238848
50	35	2.6	497	10	BE378302
51	35	2.6	501	10	BE396602
52	35	2.6	525	10	BE407307
53	35	2.6	554	10	BE792836
54	35	2.6	582	10	BM042302
55	35	2.6	605	10	BI195835
56	35	2.6	624	10	BE394122
57	35	2.6	627	10	BE302953
58	35	2.6	636	10	BE255207
59	35	2.6	659	10	BE254129
60	35	2.6	671	10	BE794312
61	35	2.6	676	10	BM042451
62	35	2.6	683	10	BM006767
63	35	2.6	686	10	BG761861
64	35	2.6	691	10	BG469125
65	35	2.6	721	10	BE299424
66	35	2.6	727	10	BE612759
67	35	2.6	733	10	BG165939
68	35	2.6	762	10	BI161016
69	35	2.6	764	10	BG481496
70	35	2.6	766	9	AL527125
71	35	2.6	768	9	AL559560
72	35	2.6	772	10	BG760541
73	35	2.6	775	10	BG397732
74	35	2.6	777	10	BG470987
75	35	2.6	779	9	AL538949
76	35	2.6	779	9	BG575348
77	35	2.6	779	9	BG575437
78	35	2.6	787	9	AL558662
79	35	2.6	793	10	BG473919
80	35	2.6	794	10	BG743980
81	35	2.6	793	10	AL528918
82	35	2.6	816	10	BF204556
83	35	2.6	827	10	BG254144
84	35	2.6	829	10	BM453887
85	35	2.6	836	9	AL521235
86	35	2.6	839	9	BE283881
87	35	2.6	850	10	BE882034
88	35	2.6	867	10	BE901896
89	35	2.6	872	10	BF797780
90	35	2.6	872	10	BF797780

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c 91 35 2.6 892 10 B1836975
92 35 2.6 892 10 BE253873
93 35 2.6 903 10 BE253873
94 35 2.6 904 10 BE682741
95 35 2.6 908 9 BE032362
96 35 2.6 919 10 AL526515
97 35 2.6 962 10 B1858840
98 35 2.6 962 10 BG340804
99 35 2.6 975 10 AL561126
100 35 2.6 976 10 BE733018
BM451205

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ALIGNMENTS

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RESULT 1
LOCUS CINS07GYI 349 bp DNA linear GSS 02-OCT-2001
DEFINITION Anopheles gambiae GSS T7 end of clone 23L04 of library Notredame1
from strain PEST of Anopheles gambiae (African malaria mosquito),
genomic survey sequence.
ACCESSION AL610380
VERSION AL610380.1 GI:15916565
KEYWORDS GSS.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidae; Anopheles.
REFERENCE 1 (bases 1 to 349)
GENOSCOPE.
AUTHORS Direct Submission
TITLE Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
2 (bases 1 to 349)
Web : www.genoscope.cns.fr)
REFERENCE 2 (bases 1 to 349)
Roth,C.W., Brey,P.T., Ke,Z. and Collins,F.H.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-2001) BBMI, Institut Pasteur, 25, rue du Dr.
Roux, Paris 75015, France
COMMENT This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
Pasteur.
FEATURES
source location/Qualifiers
1..349
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="23L04"
/clone.lib="Notredame1"
/note="end : T7"
BASE COUNT 72 a 100 c 106 g 71 t
ORIGIN

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Query Match 8.2%; Score 110.2; DB 12; Length 349;
Best Local Similarity 59.4%; Pred. No. 3.3e-20;
Matches 187; Conservative 0; Mismatches 128; Indels 0; Gaps 0;
QY 629 atgaattgagccgacatccctgagctgagcagcacatcattcatgatgagc 688
|||||
DB 32 ATGAGTTTGGCGGCCCATCCGCGGCTGTGGCGGAGACGCACATCCATTCTTCTTGG 91
QY 689 caatcgagcgaataaacaacgtgtgacacatcaattatcaagaagtgatctacgcagc 748
|||||
DB 92 CGGTGACCTTGACAAACAGAGTCTGATATATATGAGAGCGTCAATGCCATCGGTA 151
QY 749 gtttggttaaacagagcgtctgaataccgaagcgtgtgtccctggcgagcgtcgaag 808
|||||
DB 152 CGCTTTCACATCCGGGAGAGCTGTGCGGAGACGCATCATCCGATCGGTGGGCCACAG 211
QY 809 tcaacaacagcgctctgtgacgctttgtgggtgcgaagtggtctcaattacgcgcg 868

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Db 212 CTGCAAAACCCGCTCTGTGGTGAAGACGCTGATGGCGGGATATCAAGAACTGCTGAACG 271
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QY 869 gcaatggttgacgagcagcagcgtgatttcacgttcggtgattgaagcgtgacgtg 928
|||
DB 272 AAGAAACCAAGGAGGAGGAAACCGGCTGATTTCCGTTGCGTCTCAGTGGCTGATG 331
QY 929 cacaagcgcgcgacgtg 943
|||
DB 332 CCGTGCAAGCGGCACG 346

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RESULT 2
LOCUS BG606950 528 bp mRNA linear EST 17-APR-2001
DEFINITION WHE2492_E05_110Zs Triticum monococcum early reproductive apex cDNA
library Triticum monococcum cDNA clone WHE2492_E05_110, mRNA
sequence.
ACCESSION BG606950
VERSION BG606950.1 GI:13656933
KEYWORDS EST.
SOURCE Triticum monococcum.
ORGANISM Triticum monococcum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Triticum.
1 (bases 1 to 528)
Anderson,O.D., Chao,S., Dubcovsky,J., Echenique,V., Han,P.S., Hsia
,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L.,
Stamova,B. and Tong,J.C.
The structure and function of the expressed portion of the wheat
genomes - Early reproductive apex cDNA library from Triticum
monococcum
Unpublished (2001)
CONTACT: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105959773
Fax: 5105959818
Email: oanderson@w.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stragene SK primer.
location/Qualifiers
1..528
/organism="Triticum monococcum"
/cultivar="DV92"
/db_xref="taxon:4568"
/clone="WHE2492_E05_110"
/clone.lib="Triticum monococcum early reproductive apex
cDNA library"
/tissue.type="Early reproductive apex"
/dev_stage="Seven week-old plants"
/lab_host="E. coli XL0LR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; The tissue, total RNA, and
poly(A) RNA were prepared from apex at double-ridge stage
to terminal-spikelet stage during transition from
vegetative state to flower state, a cDNA library was made,
and the cDNA clones were in vivo excised at the
University of California, Davis (V. Echenique, B. Stamova
, J. Dubcovsky). Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
other authors)."
BASE COUNT 45 a 245 c 140 g 98 t
ORIGIN

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Query Match 2.9%; Score 39.2; DB 10; Length 528;
Best Local Similarity 50.0%; Pred. No. 4.3;
Matches 98; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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QY	1008	CGAGCTGGTTCGCGCGAGCGACAAATCATCATCAAGCGAACAACTCCGCGCAATT	1067
Db	205	CCGGCTGGACCTTCTTGGCGGGCGGAATCCCTCTCCGACGCCACTTCCGCTGGCGCGGAA	264
QY	1068	CTATAAACAACAACCTCTCAAGTTCAGACAGCGCGTCAAGCGGCGAGCGCGCAATGCT	1127
Db	265	CCTACACTACTTCCCGCGACACTACACGCGCGTCTGCTTCGCTTCGCGCGCTCGCTCGCT	324
QY	1128	ACCGATCGGCACTATGAGCGCGTAATGCGGTGTAACCTCTGCTACTGCTTTGCG	1187
Db	325	CCTGGCCACACCCCTTCTGCTCCTCATCTCCTCTGGGGGCTCTCGCGGCGCTGGTGGCTTCT	384
QY	1188	CGATTAACTGTCGCG	1203
Db	385	CTACATCTTCCGCGCC	400

[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 458)	Zhu, H., Lai, H., Kupfer, D., Dunlap, J. C. and Roe, B. A.	Two <i>Neurospora crassa</i> EST Databases	Unpublished (1998)	Other_ESTS: h5f02ne.r1

Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu

We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: Universal Forward Primer
High quality sequence stop: 345.

```

1.458
/organism="Neurospora crassa"
/strain="Strain 30-7 (bd; A)"
/db_xref="taxon:5141"
/clone="h5f02ne"
/clone_1lb="Neurospora crassa evening CDNA library"
/tissue_type="tissue harvested following 22hr growth in
dark"
/note="Vector: pBluescript SK-; Site_1: XbaI; Site_2:
EcoRI; See: Bell-Perdersen,D., et al. PNAS 93:13096,1996.
5' end of cDNA cloned into XbaI site of pBluescript; 3'
end of cDNA cloned into EcoRI site of pBluescript"
BASE COUNT
110 a 171 c 85 g 92 t
ORIGIN

```

Query Match	2.9%	Score 38.6	DB 9	Length 458
Best Local Similarity	48.0%	Pred. No. 5.9		
Matches 110	Conservative	0	Mismatches 119	Indels 0
			Gaps	0
Qy 717	catcaattatcaagaagctgtttgcgtatcgaagcttttgcgttaacagcgctcgaatc	776		
Db 408	CGTTCATGATGATATATATAGTTCGCCCTTGGCGAAGCTGAGGCCCTGAGACGTAGGCAATGC	349		
Qy 777	cgagcgcgtgtgtgcctttggcggcgctgcaagtcaacaacgcgcctcttgcgtacgt	836		
Db 348	CGAATTCGAGCTTCCCTCTGTGCGGCTGTGCAATTCTACACTGGGAGACCTTAGACCTTAACGA	289		

Oy	837	tttgggtggaagagtgatctacttaccgcgcgcgaattggtgttcgcgcggagcaacgcggt	886
Db	288	gcctggcgccgcgcacncttggggctggccgcctggggggagccgcctgctgcacgattacgagttccc	229
Oy	897	gatttcgcgtctcgatcttgacacgtgtgatctgcaacagcgcgcgcgtgatt	945
Db	228	agtcgattgttttcttcgcctaaagctggcatttgacgacccacgctgattgatt	180

[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 407)	Zhu H., Lai H., Kuper D., Dunlap J.C. and Roe B.A.	Two Neurospora crassa EST Databases	Unpublished (1998)	Other_ESTs: f7c01ne.r1 Other: Pwccr1.1 Doc. brn@eou University of Oklahoma.

COMMENT

Other ESTs: f7c@line.r1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: Universal Forward Primer
High quality sequence, stop: 263.

```

source
1. .407
/organism="Neurospora crassa"
/strain="Strain 30-7 (bd; A)"
/db_xref="taxon:5141"
/clone="f7c0line"
/clone_11b="Neurospora crassa evening cDNA library"
/tissue_type="tissue harvested following 22hr growth in
dark"
/note="Vector: pBluescript SK-; Site-1: XbaI; Site-2:
EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
5' end of cDNA cloned into XbaI site of pBluescript; 3'
end of cDNA cloned into EcoRI site of pBluescript"
BASE COUNT
97 a 150 c 76 g 84 t
ORIGIN

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Query Match	2.8%	Score 38.2	DB 9	Length 407
Best Local Similarity	48.0%	Pred. No. 7.2		
Matches 109	Conservative	0	Mismatches 118	Indels 0
				Caps 0
QY	719	tcaattatcaagaacgattgtcattcggaacgtttgttcgttaacaagcgccgtctgaatacgg	778	
DB	406	tccatgtatgtatgtatgtatgttgcctttggcgaacttgagagcccttgacatgttagccctccg	347	
QY	779	agcgcgcgattgtgcctcttgagcgcctgaagaatcaacaacgcgcgcctcttgcgtaacgttt	838	
DB	346	agttccgagcttgcctctgtgcgggtgtgcagatgtgcacgtggggagcgtgagcgttttaacacgc	287	
QY	839	tgggtgtgaagagtgptctcaacttaccgcgcgcgcgaattggttgaacgcgacaacgcgcgtga	898	
DB	286	tggcggcgcacatcttgggtgcccctcggggagccgctcgtgcagatttacagattccacg	227	
QY	899	tttcgcgttcgcatctgaacggtgcgattgcacaaagcgcgcgcatgat	945	

Db 226 TCGATGTTTGTGCTAAAGGTGCGATGAGAGCCAGGTGATGAT 180

RESULT 5

LOCUS B1728886

DEFINITION 1031102206.y1 C. reinhardtii CC-1690, Stress II (normalized),

ACCESSION Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.

VERSION B1728886

KEYWORDS B1728886.1 GI:15704597

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 684

Location/Qualifiers

/organism="Chlamydomonas reinhardtii"

/strain="CC-1690 wild type mt+ 21gr"

/db_xref="taxon:3055"

/clone_lib="C. reinhardtii CC-1690, Stress II (normalized)

/note="Vector: pBluescript II SK-; Site.1: EcoRI; Site.2:

XhoI; Stress condition II library, constructed by John

Davies and Jeffrey McDermott, combines cDNAs from CC-1690

cells grown to mid-log phase in TAP (NH4+ - containing)

and shifted to TAP - NO3- (24hrs); H2 production

conditions (0, 12hr, 24hr) see Mellis et al., (2000) Plant

Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +

sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr).

POLYA mRNA was purified from each sample, pooled and cDNA

synthesized. The cDNA was directionally cloned into lambda

Zap II (Stratagene) in the EcoRI (5') and XhoI (3')

sites. pBluescript II SK- plasmids were excised from the

lambda Zap clones by superinfection with Exsist

(Stratagene) phage. The library was normalized using

method 4 described in Bonaldo et al., (1996) Genome

Research 6: 791-806."

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Research 6: 791-806."

Research 6: 791-806."

Research 6: 791-806."

Research 6: 791-806."

Research 6: 791-806."

Research 6: 791-806."

RESULT 6

LOCUS A1392198/c

DEFINITION A1392198 384 bp mRNA linear EST 03-FEB-1999

ACCESSION NCMSMD6T3 substracted Mycelial Neurospora crassa cDNA clone SMD6 5'

VERSION A1392198

KEYWORDS A1392198.1 GI:4220005

SOURCE EST.

ORGANISM Neurospora crassa.

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariales; Sordariaceae; Neurospora.

AUTHORS Nelson, M.A., Kang, S., Braun, E.L., Crawford, M.E., Dolan, P.L.,

Leonard, P.M., Mitchell, J., Armijo, A.M., Bean, L., Bluyes, E.,

Cushing, T., Errett, A., Fleharty, M., Gorman, M., Judson, K., Miller, R.,

Ortega, J., Pavlova, I., Perez, J., Todisco, S., Trujillo, R.,

Valentine, J., Wells, A., Werner-Washburne, M., Yazzie, S. and Natvig

D.O.

Expressed sequences from conidial, mycelial, and sexual stages of

Neurospora crassa

Fungal Genet. Biol. 21, 348-363 (1997)

COMMENT Contact: Natvig, D.O./Nelson, M.A.

Department of Biology

University of New Mexico

Castetter Hall, Albuquerque, NM 87131, USA

Tel: 505 277 3411

Fax: 505 277 0304

Email: ngp@biology.unm.edu.

Location/Qualifiers

1. 384

/organism="Neurospora crassa"

/strain="74-OR23-1V A (F58C 2489)"

/db_xref="taxon:5141"

/clone_lib="SMD6"

/note="Subtracted Mycelial"

/sex="Mating type A"

/tissue_type="Mycelium"

/dev_stage="Mycelium"

/lab_host="E. coli"

/note="Vector: pBluescript SK (-); Site.1: EcoRI; Site.2:

XhoI; 2% sucrose for 24 hours. cDNA directionally cloned

into pBluescript SK (-) using the Uni-ZAP XR vector system

(Stratagene, La Jolla, CA). Previously identified highly

expressed clones were substracted from this library."

Research 6: 791-806."

Research 6: 791-806."

Research 6: 791-806."

RESULT 7

LOCUS B578214/c

DEFINITION B578214 150 bp mRNA linear EST 03-FEB-1999

ACCESSION NCMSMD6T3 substracted Mycelial Neurospora crassa cDNA clone SMD6 5'

VERSION B578214

KEYWORDS B578214.1 GI:4220005

SOURCE EST.

ORGANISM Neurospora crassa.

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariales; Sordariaceae; Neurospora.

AUTHORS Nelson, M.A., Kang, S., Braun, E.L., Crawford, M.E., Dolan, P.L.,

Leonard, P.M., Mitchell, J., Armijo, A.M., Bean, L., Bluyes, E.,

Cushing, T., Errett, A., Fleharty, M., Gorman, M., Judson, K., Miller, R.,

Ortega, J., Pavlova, I., Perez, J., Todisco, S., Trujillo, R.,

Valentine, J., Wells, A., Werner-Washburne, M., Yazzie, S. and Natvig

D.O.

Expressed sequences from conidial, mycelial, and sexual stages of

Neurospora crassa

Fungal Genet. Biol. 21, 348-363 (1997)

COMMENT Contact: Natvig, D.O./Nelson, M.A.

Department of Biology

University of New Mexico

Castetter Hall, Albuquerque, NM 87131, USA

Tel: 505 277 3411

Fax: 505 277 0304

Email: ngp@biology.unm.edu.

Location/Qualifiers

1. 150

/organism="Neurospora crassa"

/strain="74-OR23-1V A (F58C 2489)"

/db_xref="taxon:5141"

/clone_lib="SMD6"

/note="Subtracted Mycelial"

/sex="Mating type A"

/tissue_type="Mycelium"

/dev_stage="Mycelium"

/lab_host="E. coli"

/note="Vector: pBluescript SK (-); Site.1: EcoRI; Site.2:

XhoI; 2% sucrose for 24 hours. cDNA directionally cloned

into pBluescript SK (-) using the Uni-ZAP XR vector system

(Stratagene, La Jolla, CA). Previously identified highly

expressed clones were substracted from this library."

Research 6: 791-806."

Research 6: 791-806."

Research 6: 791-806."

LOCUS BG578214 434 bp mRNA linear EST 11-APR-2001
 DEFINITION de94b05.y1 wellcome CRC PRN3 St19 26 Xenopus laevis cDNA clone
 IMAGE:3549249.5' similar to SM:SF02.CHICK P30352 SPLICING FACTOR,
 ARGININE/SERINE-RICH 2 ; , mRNA sequence.
 ACCESSION BG578214
 VERSION BG578214.1 GI:13593278
 KEYWORDS EST
 SOURCE African clawed frog.
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 Xenopodinae; Xenopus.
 1 (bases 1 to 434)
 Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Page, D.,
 Martin, J., Wylie, T., Underwood, K., Theisling, B., Bowers, Y., Person,
 B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
 Waterston, R. and Wilson, R.
 Washu Xenopus EST project, 1999
 Unpublished (1999)
 Other ESTs: de94b05.x1
 Contact: Sandy Clifton, Ph.D.
 Washu Xenopus EST project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 Library constructed by N. Garrett, K. Ryan and A.M. Zorn
 (Wellcome/CRC Institute). DNA sequencing by: Washington University
 Genome Sequencing Center
 Clone distribution: Xenopus clones from this library are available
 through the I.M.A.G.E. Consortium/LLNL etc: info@image.llnl.gov
 Seq primer: -40RP from Gibco
 High quality sequence stop: 433.
 Location/Qualifiers
 1..434
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="IMAGE:3549249"
 /clone_1lb="Wellcome CRC PRN3 St19 26"
 /tissue_type="pooled embryos, stage 19-26"
 /lab_host="DH10B (phage-resistant)"
 /note="vector: pBSRN3; Site 1: NotI, Site 2: EcoRI; cDNAs
 were oligo-dT primed and directionally cloned. Staging
 according to Nieuwkoop and Faber. Library was constructed
 by N. Garrett, E. Bellefroid, and A.M. Zorn,
 (Wellcome/CRC Institute)."
 BASE COUNT 88 a 126 c 138 g 82 t
 ORIGIN
 Query Match 2.8%; Score 37.4; DB 10; Length 434;
 Best Local Similarity 50.9%; Pred. NO. 13;
 Matches 89; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
 Oy 678 ttatcagcagcagctgcgcgcaataaacgctgtgaccatcaatatacaagcgtgat 737
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 408 TTCATATCCCGCGCGCCGAGTCCCGGATTCGCGAGGAGCGAGCGTCTCTCCGCGAT 349
 Oy 738 tgcatacgagcgttgcgttaacagcgctcgaataacgagcggtgtgcttcctgag 797
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 348 GGGATCGGCGCGCGCGCTCGTAGCGGCGGACATCGACCTCAGCTCCGCGCGCTAACA 289
 Oy 798 cggcctgaagtaacaaacgcgcctcttcgtacacgttttggtgaggaagtc 852
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 288 CGGCCCCGCTCATAGCGTCCATCGCGTCTCGGCATCGCGCTTGTCGTGAAGAGG 234

to ref|X_051773.2 (XM_051773) deltex (Drosophila) homolog 1 [Homo
 sapiens], mRNA sequence.
 ACCESSION BM490565
 VERSION BM490565.1 GI:18611496
 KEYWORDS EST
 SOURCE chicken.
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 621)
 Porter, T.E. and Cogburn, L.A.
 ESTs from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA
 library, USDA/IRAFs Animal Genome Project
 Unpublished (2002)
 Contact: Larry A. Cogburn
 University of Delaware
 Townsend Hall, Newark, DE 19717, USA
 Tel: 302-831-1335
 Fax: 302-831-2822
 Email: cogburn@udel.edu, www.chickest.udel.edu.
 Location/Qualifiers
 1..621
 /organism="Gallus gallus"
 /strain="Commercial broiler chickens"
 /db_xref="taxon:9031"
 /clone="pgp2n.pk003.mg"
 /clone_1lb="Normalized Chicken
 Pituitary/Hypothalamus/Pineal Library (pgp2n)"
 /tissue_type="Pituitary Gland/Hypothalamus/Pineal Gland"
 /sex="Male and Female"
 /dev_stage="Embryonic (d12,d14,d19); post-hatch (1,3,5,7,9
 weeks)"
 /lab_host="E. coli EMDH10B"
 /note="vector: pCMVSPORT6; Library made from equivalent
 pools of total RNA isolated from each tissue at different
 ages. Single pass sequencing from 5'-end"
 BASE COUNT 116 a 217 c 193 g 95 t
 ORIGIN
 Query Match 2.8%; Score 37.4; DB 10; Length 621;
 Best Local Similarity 50.9%; Pred. NO. 15;
 Matches 89; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
 Oy 956 gctaccacaatcagattcgcgtatcgaagaagcgccgcaagaagctgttcgctgg 1015
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 65 GCCACCATTCGAGACGTCGTGAAGAGAGAGCCCGGTGGACGCGGTGGCCAGG 124
 Oy 1016 ttgcgcggaagccggaataatccatcaagcgcaaccttcggtccatttcctaaaaa 1075
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 125 TGGACGTGAGCGTGGACCCCTTACATCATCGACCTGCGAGTCCAGTTCGCGAGG 184
 Oy 1076 acaactctcaagtcagtcagcgagcggtcaagcgagcgagcgagcgatgac 1130
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 185 ACAAGGCGACCATGCGCGCGGTGGCAGGAACCTTTCACACCCCTCTCGGCACC 239
 RESULT 9
 LOCUS AV938950 320 bp mRNA linear EST 18-JAN-2002
 DEFINITION AV938950 K. Sato unpublished cDNA library, strain H602 adult,
 heading stage top three leaves Hordeum vulgare subsp. spontaneum
 cDNA clone ban20a24.5', mRNA sequence.
 ACCESSION AV938950
 VERSION AV938950.1 GI:18234747
 KEYWORDS EST
 SOURCE Hordeum vulgare subsp. spontaneum.
 ORGANISM Hordeum vulgare subsp. spontaneum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae
 ; Triticeae; Hordeum.
 1 (bases 1 to 320)

AUTHORS		Sato, K., Saitoh, D. and Takeda, K.	
TITLE		Barley EST sequencing project in NIG and Okayama Univ	
JOURNAL		Unpublished (2002)	
COMMENT		Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshin@genes.nig.ac.jp.	
FEATURES		location/Qualifiers	
source		1. 320 /organism="Hordeum vulgare subsp. spontaneum" /strain="H602" /db_xref="taxon:77009" /clone="bah20a24" /clone_lib="K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves" /tissue_type="top three leaves" /dev_stage="adult, heading stage" 44 a 113 c 99 g 64 t	
BASE COUNT		44 a 113 c 99 g 64 t	
ORIGIN			
Query Match		2.8%; Score 37.2; DB 9; Length 320;	
Best Local Similarity		72.7%; Pred. No. 12;	
Matches		48; Conservative 0; Mismatches 18; Indels 0; Gaps 0;	
Oy	437	cgctgcacatctgctcgaatgcgagaccacacgcgtgcgcgcgcacccacgtca	496
Db	218	CGTCACGAGTGTCTCTCCACGGGATGGCGCAACCCGCTTGCTCCACCTCAGCCTCA	277
Oy	497	tcacaa 502	
Db	278	GCACCA 283	
RESULT 10			
LOCUS		BF293584	
DEFINITION		WHE2158_E09, J1825 Triticum turgidum L. var. durum (durum wheat)	
ACCESSION		WHE2158.E09.J18, mRNA sequence.	
VERSION		BF293584	
KEYWORDS		EST.	
SOURCE		BF293584.1 GI:11224648	
ORGANISM		Triticum turgidum.	
REFERENCE		1 (bases 1 to 376) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae ; Triticeae; Triticum.	
AUTHORS		Akhunov, E., Anderson, O.D., Chao, S., Chin, A., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Kianian, P., Izzo, G.R., Miller, R., Otto, C., Rausch, C.J., Seaton, C.L., Simons, K., Tong, J.C. and Zhang, D.	
TITLE		The structure and function of the expressed portion of the wheat genomes - Whole plant cDNA library from Triticum turgidum L. var. durum	
JOURNAL		Unpublished (2000)	
COMMENT		Contact: Olin Anderson US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105959773 Fax: 510595818 Email: anders@wv.usda.gov Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratagene SK primer. location/Qualifiers	
FEATURES		1. 376 /organism="Triticum turgidum"	
source			

AUTHORS		Sato, K., Saitoh, D. and Takeda, K.	
TITLE		Barley EST sequencing project in NIG and Okayama Univ	
JOURNAL		Unpublished (2002)	
COMMENT		Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshin@genes.nig.ac.jp.	
FEATURES		location/Qualifiers	
source		1. 577 /organism="Hordeum vulgare subsp. spontaneum" /strain="H602"	

/db_xref="taxon:4513"
 /clone="HVSME10014016f"
 /clone_lib="Hordeum vulgare spike EST library HVCNDA0012
 (Fusarium infected)"
 /tissue_type="Spike"
 /lab_host="TJC121"
 /note="vector: pBluescript SK(-); Site1: EcoRI; Site2:
 XhoI; Plants were grown at the University of Minnesota in
 the GJ Muehlbauer lab; spikes were harvested and snap
 frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium
 graminearum inoculation (Heinen). In the TJ Close lab at
 the University of California, Riverside, total RNA was
 prepared from each sample pool, equal quantities of all
 eight RNA pools were combined, poly(A) RNA was purified
 from the mixture, one primary unamplified cDNA library was
 made, and 1 million pfu were in vivo excised to give
 pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi
). Phagemids were plated and picked at the Clemson
 University Genomics Institute (CUGI) (Begum, Palmer,
 Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
 sequencing and sequence analysis were performed at CUGI
 (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
 The sequence has been trimmed to remove vector sequence
 and contains a minimum of 100 bases of phred value 20 or
 above. For more details on library preparation and
 sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders Also
 see Close TJ, Wing R, Kleinhoft A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 188 a 295 c 204 g 202 t 1 others

ORIGIN

Query Match 2.7%; Score 36.6; DB 10; Length 890;
 Best Local Similarity 52.3%; Pred. No. 29;
 Matches 81; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 961 cacatcagatccgtatcgaagagcgagcaagaagctgttcggtggtg 1020
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 265 CTCACACCCGGTGGCGCTTCGAGAACCCCGCAAGAGCTCGCGCTGTCGCC 324

Qy 1021 ccgacgcgcgacaatactcatcagcgacacactctgcgcatctccataaataa 1080
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 325 ACCAACACCGCAGACGGCTTCGTCGACCCCTTCGTCGTATGCGATATCATCTGC 384

Qy 1081 ctctcaagttcagacagcgctcaagcgcgga 1115
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 385 CACCGCGCGCCGAGAACGCCGTAAAGTCCGCCAA 419

RESULT 17
 BE360609/c 216 bp mRNA linear EST 20-JUL-2000
 LOCUS
 DEFINITION DGI_64_H11.g1_A002 Dark Grown 1 (DGI) Sorghum bicolor cDNA, mRNA
 sequence.

ACCESSION BE360609
 VERSION BE360609.1 GI:9302166
 KEYWORDS EST.
 SOURCE sorghum.
 ORGANISM Sorghum bicolor

REFERENCE
 AUTHORS Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 216)
 Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
 L. H.

TITLE An EST database from Sorghum: dark-grown seedlings
 JOURNAL Unpublished (2000)
 COMMENT Contact: Cordonnier-Pratt MM
 Department of Botany

The University of Georgia
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 542 1805
 Email: mmpattee@uga.edu
 Sequences have been trimmed to exclude polyA, vector and regions
 below Phred quality 16. The threshold for highest quality sequence
 is 20.
 Seq primer: PolyTMix
 High quality sequence start: 4
 High quality sequence stop: 207
 POLYA=Yes.
 Location/Qualifiers

FEATURES

source

1..216
 /organism="Sorghum bicolor"
 /db_xref="taxon:4558"
 /clone_lib="Dark Grown 1 (DGI)"
 /note="Organ: 5-day-old dark-grown seedlings; Vector:
 lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
 made from poly-A RNA in the cloning vector lambda Zap II.
 Clones to be sequenced were prepared by mass excision."

BASE COUNT 44 a 70 c 80 g 22 t

ORIGIN

Query Match 2.7%; Score 36.4; DB 10; Length 216;
 Best Local Similarity 51.2%; Pred. No. 17;
 Matches 85; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy 1036 tactcatcagcgacacacactctggcattctcctaataaactcttaagtacg 1095
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 215 TCTCTGATCTTGGGCGCAGAGGCTCGCCCTCGCGGTCGTCCTCTCATGCGGCC 156

Qy 1096 acagcgctcaacgagcgagcgacgcgcatgttacccgacattatgagcgtaaty 1155
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 155 GCGCGCGCCCATGTCGGCGCCGCCCTGTGACATCTTGGCGATGATGGGTTGCAAG 96

Qy 1156 ccgttgacatctgactactctgttcttgcgcgatlaatcg 1201
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 95 CGACTCGACCTCTTCATCTGCTCGAATCGTCGCCCTCGCGG 50

RESULT 18
 BE424405 328 bp mRNA linear EST 24-JUL-2000
 LOCUS
 DEFINITION WHE0078.E09.J1825 wheat endosperm cDNA library Triticum aestivum
 cDNA clone WHE0078.E09.J18, mRNA sequence.

ACCESSION BE424405
 VERSION BE424405.1 GI:9422248
 KEYWORDS EST.
 SOURCE bread wheat.
 ORGANISM Triticum aestivum

REFERENCE
 AUTHORS Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Triticum.
 1 (bases 1 to 328)
 Altenbach, S., Anderson, O.D., Chao, S., Gall, G., Han, P.S., Hsia
 C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and
 Tong, J.C.

TITLE The structure and function of the expressed portion of the wheat
 genomes - Endosperm cDNA library
 JOURNAL Unpublished (2000)
 COMMENT Contact: Olin Anderson
 US Department of Agriculture, Agricultural Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105585773
 Fax: 5105585818
 Email: oanderson@pw.usda.gov
 Sequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: Stratagene SK primer.
 Location/Qualifiers


```

/lab_host="E. coli SOLR"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/Note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
greenhouse. Spikes at 5, 10 and 15 DAP were harvested,
total RNA and poly(A) RNA were prepared, a cDNA library
was made, and the cDNA clones were in vivo excised to
give plasmid phagemids in the T7 Close lab (Choi,
Close, Fenton) at the University of California,
Riverside. Plasmid DNA preparations and DNA sequencing
were performed in the OD Anderson lab (all other authors
)."
```

BASE COUNT 131 a 117 c 118 g 94 t

ORIGIN

```

Query Match 2.7%; Score 36.2; DB 10; Length 460;
Best Local Similarity 50.3%; Pred. No. 28;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 152 tcaaaagcccaagtcgtgttggaagcaaaagacccggcgtagtattactgcgc 211
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 191 TCAAGCATGTGTGACAAAGATCTTGACGACGAAACAAAGGTCTTGTGGACACAGTGC 250
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 212 cggcttcaggcaaatcgccgctattcaccgtgagcaagcgcgctacttcagtcagtcg 271
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 251 AACTGGCAATCAAAATCTTGCGATTCAGTGTGTGACAGGTTCCAGCCATGCGACCG 310
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 272 tgattgcggttgaagcaagcaaatcgatcgaacgtctacgtcgaagcgcg 328
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 311 AGGTACAGCTGGGTACTACACTTACATGATAGAGACGGCTACAGCCATAGCAC 367
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 21
BE590713 460 bp mRNA linear EST 18-AUG-2000
LOCUS BE590713
DEFINITION WHE0856_A07_A14Zs Wheat 20-45 DAP spike cDNA library Triticum
aestivum CDNA clone WHE0856_A07_A14, mRNA sequence.
ACCESSION BE590713
VERSION BE590713.1 GI:9845786
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum

REFERENCE
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat
genomes - 20-45 DAP spike cDNA library
Unpublished (2000)
JOURNAL Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@w.usda.gov

COMMENT
TITLE The structure and function of the expressed portion of the wheat
JOURNAL genomes - 20-45 DAP spike cDNA library
COMMENT Unpublished (2000)
CONTACT: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@w.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: StrataGene SK primer.

FEATURES

source
1..460
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0856_A07_A14"
/clone_lib="Wheat 20-45 DAP spike cDNA library"
/tissue_type="Spike and seed"
/dev_stage="Adult plant"

```

/lab_host="E. coli SOLR"
/Note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
greenhouse. Spikes at 20 DAP and seeds at 30 to 45 DAP
were harvested, total RNA and poly(A) RNA were prepared, a
cDNA library was made, and the cDNA clones were in vivo
excised to give plasmid phagemids in the T7 Close lab
(Choi, Close, Fenton) at the University of California,
Riverside. Plasmid DNA preparations and DNA sequencing
were performed in the OD Anderson lab (all other authors
)."
```

BASE COUNT 129 a 117 c 114 g 100 t

ORIGIN

```

Query Match 2.7%; Score 36.2; DB 10; Length 460;
Best Local Similarity 50.3%; Pred. No. 28;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 152 tcaaaagcccaagtcgtgttggaagcaaaagacccggcgtagtattactgcgc 211
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 227 TCAAGCATGTGTGACAAAGATCTTGACGACGAAACAAAGGTCTTGTGGACACAGTGC 286
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 212 cggcttcaggcaaatcgccgctattcaccgtgagcaagcgcgctacttcagtcagtcg 271
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 287 AACTGGCAATCAAAATCTTGCGATTCAGTGTGTGACAGGTTCCAGCCATGCGACCG 346
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 272 tgattgcggttgaagcaagcaaatcgatcgaacgtctacgtcgaagcgcg 328
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 347 AGGTACAGCTGGGTACTACACTTACATGATAGAGACGGCTACAGCCATAGCAC 403
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 22
BE75489 475 bp mRNA linear EST 20-SEP-2000
LOCUS BE75489
DEFINITION MY-01-E-04 Pinifestansmy Phytophthora infestans cDNA, mRNA sequence.
ACCESSION BE75489
VERSION BE75489.1 GI:10229032
KEYWORDS EST.
SOURCE potato late blight agent.
ORGANISM Phytophthora infestans

REFERENCE
AUTHORS Kamoun,S., Hirber,P.T., Sobral,B.W.S., Nuss,D. and Govers,F.
Initial assessment of gene diversity for the oomycete pathogen
Phytophthora infestans based on expressed sequences
Fungal Genet. Biol. 28 (2), 94-106 (1999)
JOURNAL
MEDLINE 20056376
COMMENT Contact: Govers F
Laboratory of Phytopathology
Wageningen University
Bilthoven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands
Tel: 31 317 483 138
Fax: 31 317 483 412
Email: Francine.Govers@medew.fyto.wau.nl.

FEATURES

source
1..475
/organism="Phytophthora infestans"
/strain="DDR7602, A1 mating type"
/db_xref="taxon:4787"
/clone_lib="Pinifestansmy"
/dev_stage="4-week old vegetative, non-sporulating
mycelium in synthetic medium"
/lab_host="E. coli, strain DH5-alpha"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; Total
RNA was isolated from mycelium of P. infestans DDR7602
cultured for 4 weeks in synthetic medium. EST clones were
named by their position in the microtiter plate, preceded
by the prefix MY (for mycelial) and the successive number
of the microtiter plate (e.g. MY-06-A-04)."

BASE COUNT 109 a 149 c 123 g 84 t 10 others

Db 316 TTCCAGCGGAGCGCCGAGCAGCAGCGCCGCCGAGATGACACCGAAGTGT 257
 QY 476 tggcgcgcacccctcgtcatcaagaagccgcgaagacttcaacgcgcctgt 535
 Db 256 TCATTGCGGTCCCGCAGCAGCGTGTGTGACGAGCCGAGCGCCGAGCAGCGCGC 197
 QY 536 tggattagccgcctgacgca 558
 Db 196 TTGAAGCTAGTACCGCCGCGA 174

RESULT 34
 B1949252 574 bp mRNA linear EST 19-OCT-2001
 LOCUS B1949252
 DEFINITION HVSMEL0013A08f Hordeum vulgare spike EST library HVCDNA0012
 (Fusarium infected) Hordeum vulgare cDNA clone HVSMEL0013A08f, mRNA
 sequence.
 ACCESSION B1949252
 VERSION B1949252
 KEYWORDS B1949252.1 GI:16290354
 SOURCE EST.
 ORGANISM Hordeum vulgare
 Barley.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 1 (bases 1 to 574)
 Wing, R., Muehlbauer, G.J., Close, T.J., Kleinbols, A., Wise, R., Heinen
 S., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T.,
 Simmons, U., Fenton, R.D., Malatrasi, M., Choi, D.W., Oates, R. and Main
 D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Fusarium infected Morex spike cDNA library
 unpublished (2001)
 JOURNAL Contact: Wing RA
 COMMENT Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Total hg bases = 227
 Seq primer: AATTAACCTCCTCCTCAAGG
 High quality sequence start: 61
 High quality sequence stop: 465.

FEATURES
 SOURCE Location/Qualifiers
 1..574
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSMEL0013A08f"
 /clone_lib="Hordeum vulgare spike EST library HVCDNA0012
 (Fusarium infected)"
 /tissue_type="Spike"
 /lab_host="TJC121"
 /note="Vector: Bluescript SK(-); Site:1: EcoRI; Site:2:
 XhoI; Plants were grown at the University of Minnesota in
 the GJ Muehlbauer lab; spikes were harvested and snap
 frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium
 graminearum inoculation (Heinen). In the TJC Close lab at
 the University of California, Riverside, total RNA was
 prepared from each sample pool, equal quantities of all
 eight RNA pools were combined, poly(A) RNA was purified
 from the mixture, one primary unamplified cDNA library was
 made, and 1 million pfu were in vivo excised to give
 Bluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi
). Phagemids were plated and picked at the Clemson
 University Genomics Institute (CUGI) (Begum, Palmer,
 Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
 sequencing and sequence analysis were performed at CUGI
 (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
 The sequence has been trimmed to remove vector sequence
 and contains a minimum of 100 bases of phred value 20 or

above. For more details on library preparation and
 sequence analysis see
<http://www.genome.clemson.edu/projects/barley>. To order
 this clone see <http://www.genome.clemson.edu/orders> Also
 see Close T.J., Wing R., Kleinbols A., Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (<http://wheat.pw.usda.gov/ggpages/pqgn/31/cover.html>)"

BASE COUNT 178 a 128 c 137 g 123 t 8 others

ORIGIN

Query Match 2.7%; Score 35.8; DB 10; Length 574;
 Best Local Similarity 49.7%; Pred. No. 40;
 Matches 88; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 152 tcaaaaaggccaaagtgtgtttgaagacaaaagaatccggcgtagtattactgcgc 211
 Db 214 TCAAGCAGCGGTGACAGGATCTTGATGAAGCAAGAGCTCTTGCGATCAAGGNN 273
 QY 212 cggcttcaggcaaatccgcgcgtattccgcgtgycgaagaagcgctacttcgtcgtc 271
 Db 274 CAACCTCAATCAAGATCTGTGGCATTCTGCTGTTCAAGGTTCCAGCCATGACGCCG 333
 QY 272 tgaatgcgttgaagcaagcaagcaatcgagttcgacgtactgacgtgaagcgc 328
 Db 334 AGCTCACAGCTGGTGTACTCACTTACATGATGATGACAGCATACACCATATGAC 390

RESULT 35
 BG579193/c
 LOCUS BG579193
 DEFINITION d124f02.y1 Wellcome CRC PRN3 St10.5 Xenopus laevis cDNA clone
 IMAGE:3558290.5' similar to SW:SF02.CHICK P30352 SPLICING FACTOR,
 ARGININE/SERINE-RICH 2 ; , mRNA sequence.
 ACCESSION BG579193
 VERSION BG579193
 KEYWORDS BG579193.1 GI:13594267
 SOURCE EST.
 ORGANISM African clawed frog.
 Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 Xenopodinae; Xenopus.
 1 (bases 1 to 615)
 Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Page, D.,
 Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person
 B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
 Waterston, R. and Wilson, R.
 WashU Xenopus EST project, 1999
 Unpublished (1999)
 Contact: Sandy Clifton, Ph.D.
 WashU Xenopus EST project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estelw@wustl.edu
 Library constructed by N. Garrett, P. Lemaire, A.M. Zorn, and J.B.
 Gurdon (Wellcome/CRC Institute). DNA Sequencing by: Washington
 University Genome Sequencing Center
 Clone distribution: Xenopus clones from this library are available
 through the I.M.A.G.E. Consortium/LMWL at: info@image.llnl.gov
 Seq primer: -40RP from Gibco
 High quality sequence stop: 474.

FEATURES
 SOURCE Location/Qualifiers
 1..615
 /organism="Xenopus laevis"
 /cultivar="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="IMAGE:3558290"
 /clone_lib="Wellcome CRC PRN3 St10.5"
 /tissue_type="embryo, stage 10.5"
 /lab_host="DHI0B (phage-resistant)"
 /note="Vector: pBSRN3; site_1: NotI; site_2: EcoRI; CDNAS

	RESULT	40						
	LOCUS	A1399239	506 bp	mRNA	linear	EST-08-FEB-1999		
	DEFINITION	MCM10F2T3 Westergaards Neurospora crassa cDNA clone W10F2 5', mRNA sequence.						
	ACCESSION	A1399239						
	VERSION	A1399239.1						
	KEYWORDS	GI:4242324						
	SOURCE	EST.						
	ORGANISM	Neurospora crassa.						
		Neurospora crassa.						
		Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Eurotiiales; Sordariaceae; Neurospora.						
	REFERENCE	1 (bases 1 to 506)						
	AUTHORS	Nelson,M.A., Kang,S., Braun,E.L., Crawford,M.E., Dolan,P.L., Leonard,P.M., Mitchell,J., Armijo,A.M., Bean,L., Bluesies,E., Cushing,T., Eretell,A., Flehardt,A., Gorman,M., Judson,K., Miller,R., Ortega,J., Pavlova,I., Perez,J., Todisco,S., Trujillo,R., Valentine,J., Wells,A., Werner-Washburne,M., Yazzie,S. and Natvig,D.O.						
	TITLE	Expressed sequences from conidial, mycelial, and sexual stages of Neurospora crassa						
	JOURNAL	Fungal Genet. Biol. 21, 348-363 (1997)						
	MEDLINE	97435549						
	COMMENT	Contact: Natvig,D.O./Nelson,M.A. Department of Biology University of New Mexico Casterlet Hall, Albuquerque, NM 87131, USA Tel: 505 277 3411 Fax: 505 277 0304 Email: npgebiology.unm.edu.						
	FEATURES	Location/Organisms						
	Source	1..506						
		/organism="Neurospora crassa"						
		/strain="74-OR23-IV A (FGSC 2489)"						
		/db_xref="taxon:5141"						
		/clone="W10F2"						
		/clone_lib="Westergaards"						
		/sex="Mating type A"						
		/tissue_type="Unfertilized sexual tissue"						
		/dev_stage="Unfertilized sexual stage"						
		/lab_host="E. coli"						
		/note="Vector: pBluescript SK (-); Site.1: EcoRI; Site.2: XhoI; Westergard's medium (Nitrogen limiting). Floating mycelial mats grown at 25C for 36 hours. CDNA directionally cloned into pBluescript SK(-) using the Uni-ZAP XR vector system (Stratagene, La Jolla, CA)." 129 t 4 others						
	BASE COUNT	105 a 136 c 132 g 129 t						
	ORIGIN							
	Query Match	2.6%; Score 35.6; DB 9; Length 506;						
	Best Local Similarity	48.2%; Pred. No. 43;						
	Matches	95; Conservative 0; Mismatches 102; Indels 0; Gaps 0;						
OY	100	gaagaatatgctcgagatgcgccctcgaataacaaagaaagtgtgaagccgtcaaaaa 159						
Db	27	GAGGCAATGGCGCTTCAGCTCCAGTTGATTCCCCAGAGCGTAAGAAGCTCCGTCAA 86						
OY	160	ggccaagtgcgtgttttgaaacaanaagaattccggcgtagtatattactgcgcgccta 219						
Db	87	GGGCGTGTCGAACGGGAGAACANGCTGCCCTGCACCATCTCNMGCHCCGCCCATC 146						
OY	220	ggcaaatcgcgcgtattaccgcgttggcgaaaaggcgcgtacctcaagttaagtcgatgtgc 279						
Db	147	GCTAAGGGGGGGGCGGTATCCATGCGCCGCTTAAGGCGACCGGAAGATGACCATTTGCT 206						
OY	280	gttgaaggcaacgacga 296						
Db	207	GTTAAAGCACGAMAACA 223						

[illegible]

Tel: +44 131 650 5760
Fax: +44 131 670 5450
Email: mark.blaaxter@ed.ac.uk
The library was prepared by Richard Grencis, Manchester University,
Manchester. Sequencing was performed by the Pathogen Sequencing
Unit, Sanger Centre, Cambridge, UK (Neil Hall, Mike Quail & Bart
Barrell). The sequence contained a Polya tail (trimmed)

```

source
1. 580
location/qualifiers
/organism="Friticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"

```

